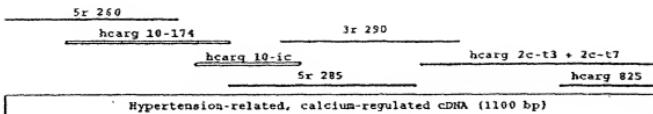


A



B

Y

-111 GACAGGAGCCACAGGCCAGCTACCGGCCCTAGGTTCTCCAGGTGAGAGGGCG -80

GTAAAGGCTCTGGTTGTATTTGAAATGCTACTGGTTAGGACCTCTTCGGACTGTCAGAAACGGGAAAGG -1

ATG TCT GCT TTG CGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly 60

CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG AGC GCC GTG GCT CAG CTC TTG 120

Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu

AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TIG RAA CTT GTA GTC GGG GCC CTG CAT 180

Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Gln Ala Leu His

GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240

Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu

CGT CTG GCC GTC CTG CGC GGC ACA AAC ACC CTC CAG CAG GCT CTC CGG CTG CCC 300

Arg Leu Ala Val Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro

CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT ATT CCT CAG 360

Pro Ala Leu Lys Asp Leu Lys Phe Gln Gln Gln Leu Gln Ile Pro Gln

GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCTT CTC GAC TCT 420

Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser

GTA GCC CAA CAG GGA TCC TCG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480

Val Ala Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp

GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CGG AGT GTT CTC ATG CAG CTG 540

Val Ala Ile Ser Thr Ser Ala Gln Arg Ser Gln Pro Ser Val Leu Met Gln Leu

AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600

Lys Leu Thr Asp Gly Ser Ala His Arg Phe Gln Val Pro Ile Ala Lys Phe Gln Glu Leu

CGG TAC AGT GTC TCC AGG GCT CTT AAC GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660

Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Glu Lys Lys Cys Glu Arg

AAA CTG CAG GNC TGA CTGAAACCTGGTACTGTGGGTGCTGAGCTGGTACAGAACACAGCCCCCCTACTGGTGA 734

Lys Leu Gln Asp TER

TGAGCCCCAACCTCATGAGGGCTCTGGTGTGAGAACGTTTAAAGTGAARAGACAGCGGGACTTTCAGGTTTGTGTTA 813

ATGAGTCACACGCTGGGCGAGGGTGGCACAGTTATACATCTGAGCCCTGGAGACTGAGGGCTGGAGATGGAGCTGA 892

AGCTGGGCTGGCTTCATAGTGGGCTCAGTGTGCAATTAAAAGAGTAAAGCAACTTAAAAA.....AAA 969

FIGURE 1

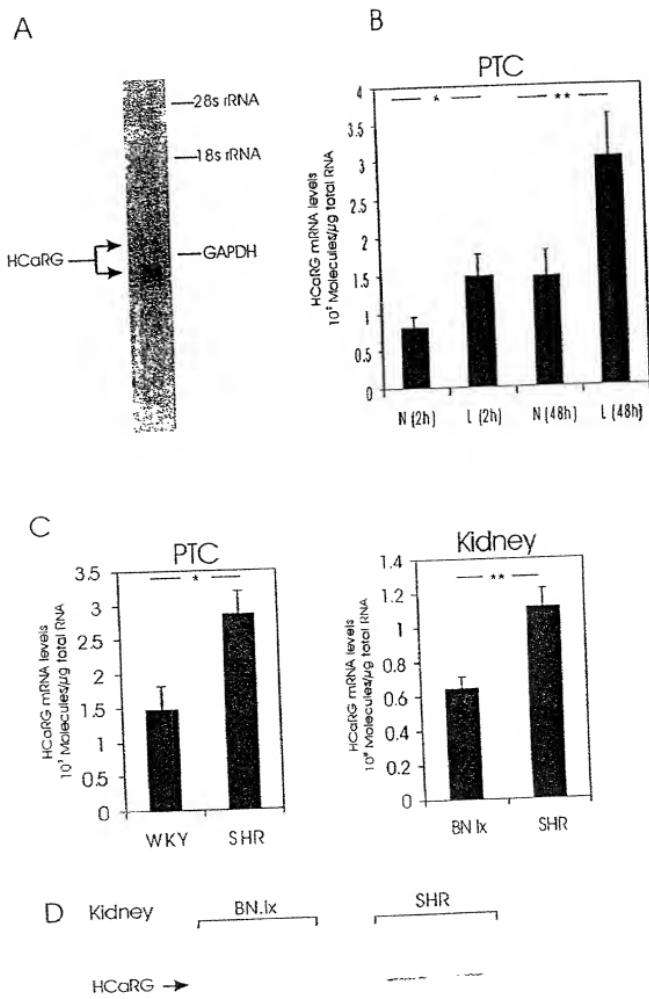


FIGURE 2

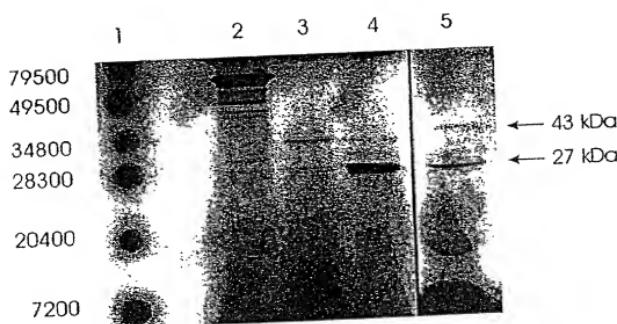


FIGURE 3

2052m089560

rHCaRG	MSA [GAPAPY] SPP PAPSSS MSA [GAPAPY] SPP PAPSSS	50
hHCaRG	MSA [GAPAPY] SPP PAPSSS MSA [GAPAPY] SPP PAPSSS	50
rHCaRG	ELKIVVGIHL GAD CREAIVQ LURFVSSIQ GAD CREAIVQ	100
hHCaRG	ELKIVVGIHL GAD CREAIVQ LURFVSSIQ GAD CREAIVQ	100
rHCaRG	PASLKPDPFQ EFLQELCIPQ DILGDDIASLA PISLKPDPFQ EFLQELCIPQ DILGDDIASVV	150
hHCaRG	PASLKPDPFQ EFLQELCIPQ DILGDDIASLA PISLKPDPFQ EFLQELCIPQ DILGDDIASVV	150
rHCaRG	HVSIFRWRVD VAIStSIAQSR SLOPSVLMQL HVAIFRWRVD VAIStSIAQSR SLOPSVLMQL	200
hHCaRG	HVSIFRWRVD VAIStSIAQSR SLOPSVLMQL HVAIFRWRVD VAIStSIAQSR SLOPSVLMQL	200
rHCaRG	RYSVALVKE YAE LEVNCER KIQD RYSVALVKE YAE LEVNCER KIQD	224
hHCaRG	RYSVALVKE YAE LEVNCER KIQD RYSVALVKE YAE LEVNCER KIQD	224

FIGURE 4

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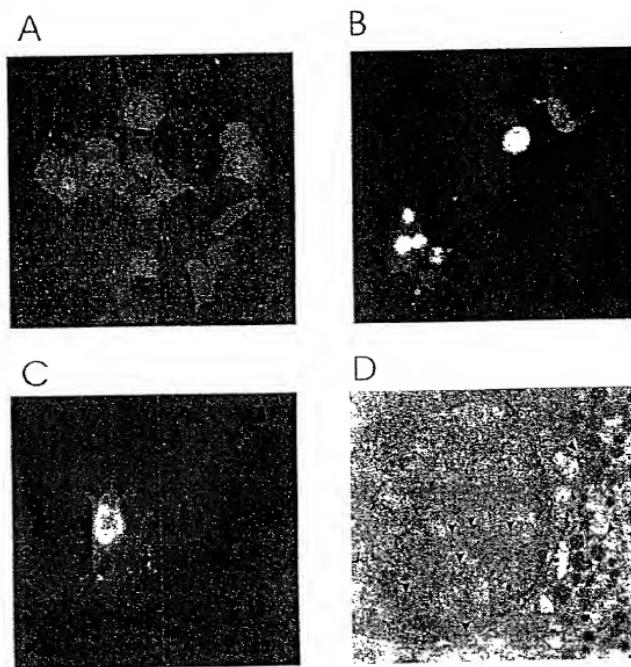
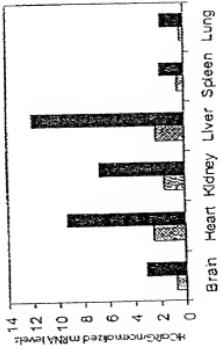
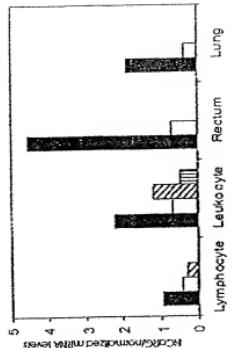


FIGURE 5

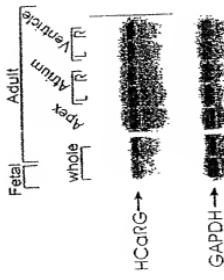
A Fetal/Adult



C Normal/Cancerous



B HEART



D Tumor/Normal

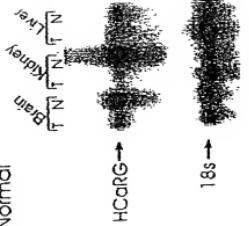


FIGURE 6

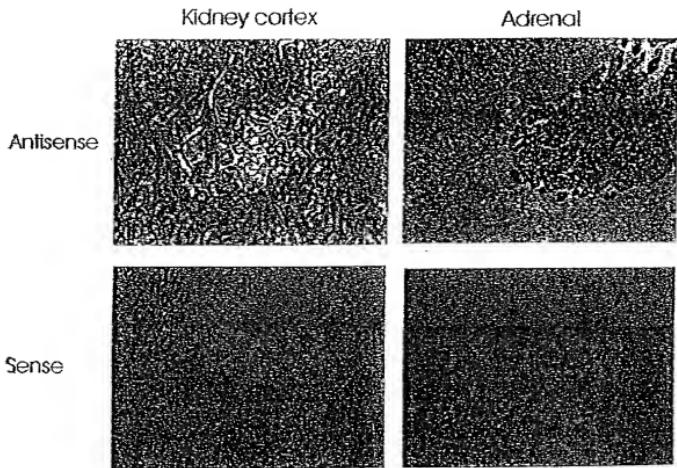
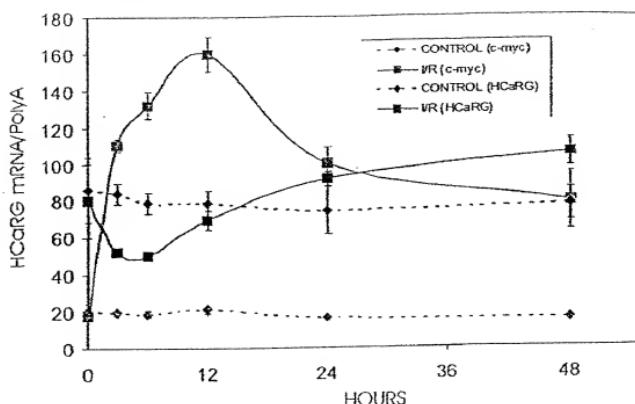
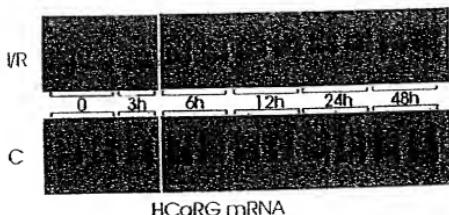


FIGURE 7

A Medulla



B Cortex



C Cortex

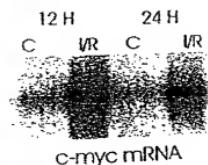
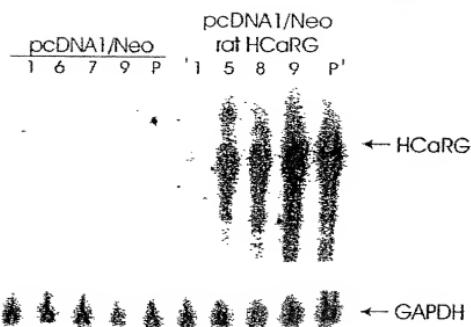


FIGURE 8

A



B

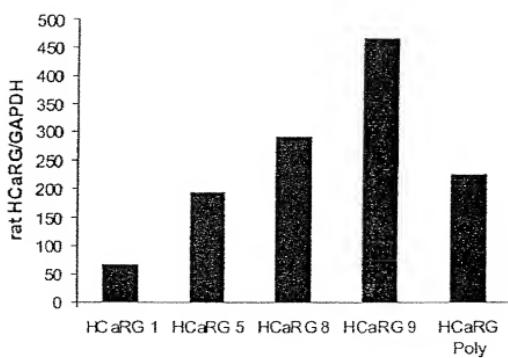
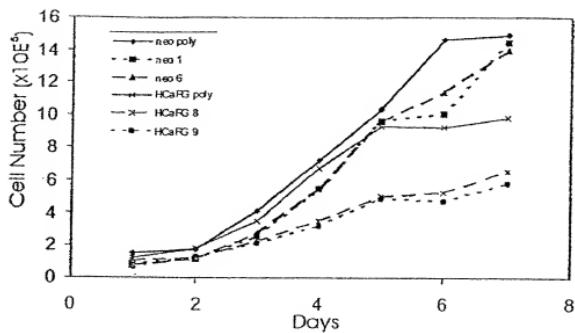


FIGURE 9

A



B

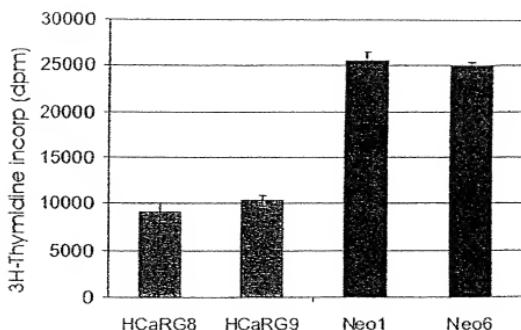


FIGURE 10

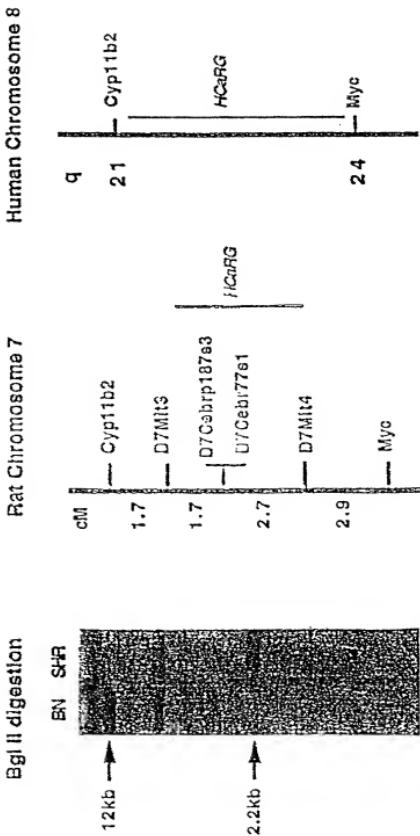


FIGURE 11